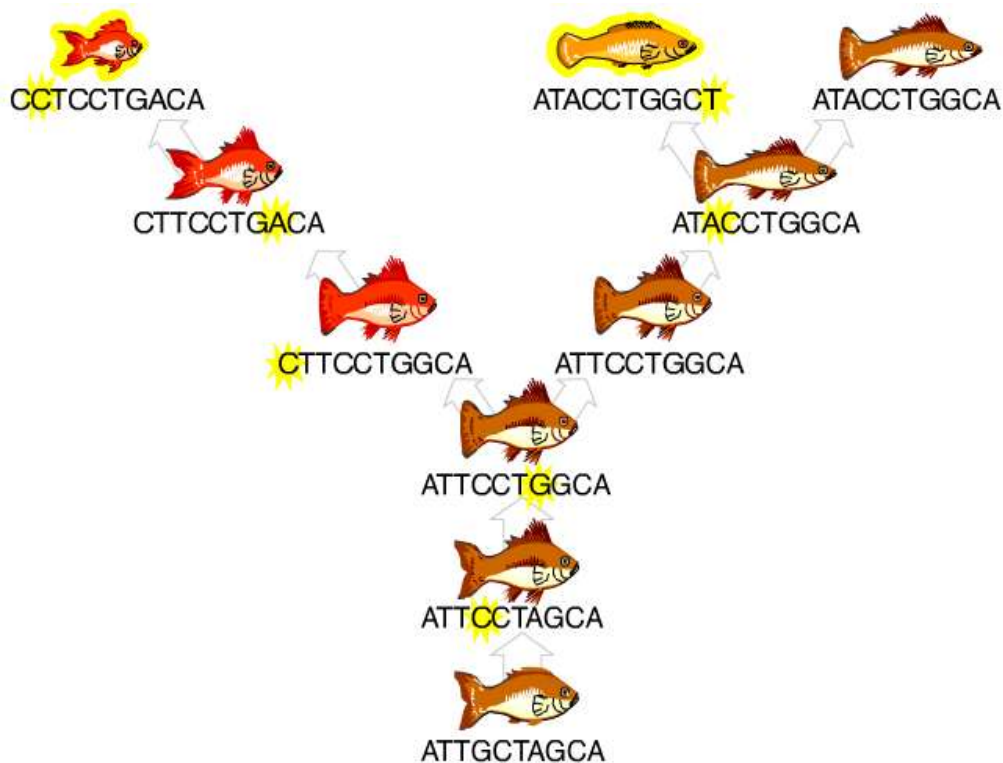


Name _____ Period _____

Protein Sequence Analysis Activity

Pre-Lab Question:

Explain the types of mutations that most likely account for gradual changes in the amino acid sequences of similar proteins in different organisms.



previous replay next

1 of 5

Researchers compare molecules, as well as anatomical structures, to classify organisms and reconstruct evolutionary trees. [DNA](#) and [RNA](#) base sequences from closely related species are similar. As you can see in this diagram, there are greater differences in sequence between species that are less closely related—those whose evolutionary paths diverged a longer time ago.

Differences in protein amino acid sequences reflect differences in DNA base sequences. This activity allows you to compare amino acid sequences of proteins from different species and use them to deduce evolutionary relationships.

1. Click on the Questions window and answer Question 1.

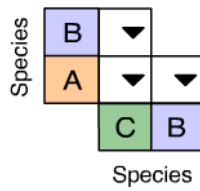
At left are three comparisons of amino acid sequences of the electron transport protein cytochrome c from three species of animals, designated by the capital letters A, B, and C. Each amino acid in the proteins is represented by a small letter. The differences in amino acid sequence are highlighted. (Note that for the purposes of this activity, the data are simplified.)

2. For each one of the three comparisons, count the differences in the amino acid sequence. Then click on the appropriate arrow in the chart to choose the correct number of differences.

Species A:	a	v	l	l	g	m	f	a	s	y	t	h	k	k	s	d	c	t	c	r
Species B:	v	v	l	i	f	p	w	d	c	y	t	r	k	r	s	e	c	t	c	h

Species A:	a	v	l	l	g	m	f	a	s	y	t	h	k	k	s	d	c	t	c	r
Species C:	a	v	l	l	g	f	f	a	w	y	t	h	r	k	s	d	c	t	c	r

Species B:	v	v	l	i	f	p	w	d	c	y	t	r	k	r	s	e	c	t	c	h
Species C:	a	v	l	l	g	f	f	a	w	y	t	h	r	k	s	d	c	t	c	r



Number of differences
in amino acid sequences

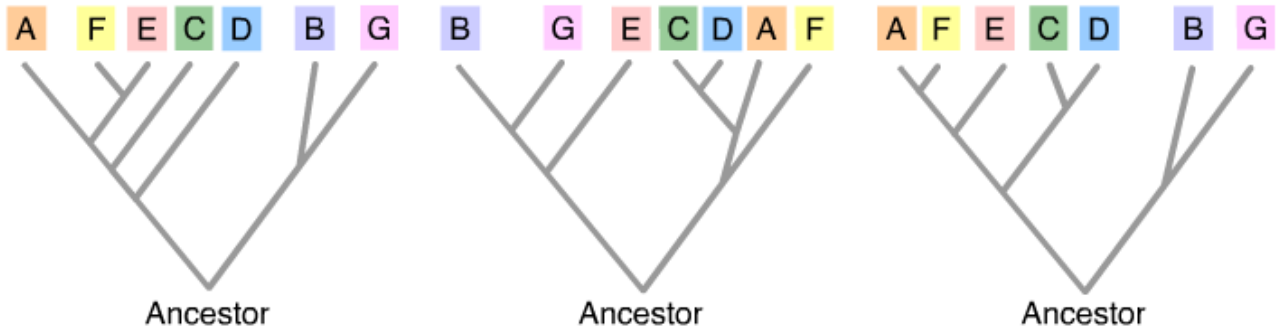
1. How many differences are there among...?

Species A & C _____ Species A & B _____ Species B & C _____

Species A:	a v l l g m f a s y t h k k s d c t c r l g l f p
Species B:	l p f i g f g i s y t q k t y e c d c r l m l f w
Species C:	a v l l g m f p c y t t k k s d s d c r l g l f p
Species D:	a v l l g m f p s y t t k k s d s d t r l g l f p
Species E:	a v l i g m f p s y t h k k s d s t c r l g l f p
Species F:	a v l l g m f g s y t h k k s d c t c r l g l f p
Species G:	l p f i g v g m s y t r k r s e c d c t l f l f w

Species	B						
	C						
	D						
	E						
	F						
	G						
	A	B	C	D	E	F	
	Species						

2. Fill in the number of differences among the species using the data provided.



3. Given the data on the previous page, which of the phylogenetic trees shown above best reflects the evolutionary and taxonomic relationships among these seven species?

Justify your response by explaining the accuracies in the correct tree and the inaccuracies of the other 2 trees.

Industry & Medicine Application

Protein comparisons are also useful for studying differences and similarities within the same species. Similarities in certain proteins may indicate organisms from a specific region of the world or those belonging to a particular lineage. Scientists can use protein comparisons to identify organisms originating from a particular ancestor. In many instances this type of analysis can be used to determine the origin of bacteria that produce food poisoning. Now we will investigate the source of food poisoning bacteria identified with hamburgers sold at three restaurants. The restaurants purchased their hamburgers from three different suppliers who used meat from one meat processing plant. The restaurants and hamburger suppliers claim the bacterial contamination occurred at the meat processing plant.

To identify the source of bacterial contamination, we will use **variations in the amino acid sequence of the tryptophan synthetase A protein**. Geneticists have identified three regions (sequences) of the tryptophan synthetase A gene having predictable base pair mutations. These spontaneous mutations are passed on through binary fission and are generally unique to a recent lineage of a particular bacterium. They affect the protein by substituting the amino acids on the point mutation site.

Sequences in Bacteria from Meat Plant

Sequence 1:	T Y L L S R A G V T G A
Sequence 2:	P P L Q G F G I S A P D
Sequence 3:	G A I S G S A I V Y I I

Sequences in Bacteria from Restaurant 1

Sequence 1:	T Y L L S R A G V T G A
Sequence 2:	P P L Q G F G I S A P D
Sequence 3:	G A I S G S A I V Y I I

Sequences in Bacteria from Restaurant 2

Sequence 1:	T C L L S R A G V T G A
Sequence 2:	P P L Q R F G I S A P D
Sequence 3:	G A I S D S A I V Y I I

Sequences in Bacteria from Restaurant 3

Sequence 1:	T Y L R S R A G V I G A
Sequence 2:	P P L Q G F V I S A P D
Sequence 3:	G A I L C S A I V Y I I

4. Fill in the data table using the data on the previous page

	Number of differences in amino acids			Total number of differences in amino acids
Comparison	Sequence 1	Sequence 2	Sequence 3	
Meat Plant Vs. Restaurant 1				
Meat Plant Vs. Restaurant 2				
Meat Plant Vs. Restaurant 3				
Restaurant 1 Vs. Restaurant 2				
Restaurant 1 Vs. Restaurant 3				
Restaurant 2 Vs. Restaurant 3				

5. What conclusions can you make about the origins of the bacterial contamination for the three restaurants?

6. Why does the tryptophan synthetase A amino acid sequence differ between bacteria on hamburgers 1 and 2 if the bacteria are from the same origin?

7. What other types of testing could be done to confirm with little doubt the origin of the food contamination?